

ABSTRACT OF THE DISCLOSURE

Methods and apparatuses for deriving the sequence of an oligomer. In one exemplary method for deriving the sequence of a polypeptide, a predetermined set of mass/charge values for amino acid sequences is stored. An abundance value from mass spectrum data for each mass/charge value in the predetermined set is determined to produce a plurality of abundance values. A first ranking, based on the plurality of abundance values, is calculated for each sequence of a set of amino acid sequences having a first number of amino acids. A second ranking, based on the plurality of abundance values, for each sequence of a set of amino acid sequences having a second number of amino acids is calculated. A cumulative ranking, based on the first ranking and the second ranking, is calculated for each sequence of a set of amino acid sequences having at least the second number of amino acids.